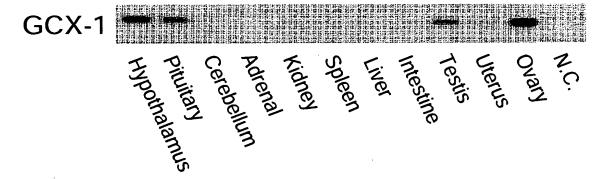
10/542161

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Fig. 1

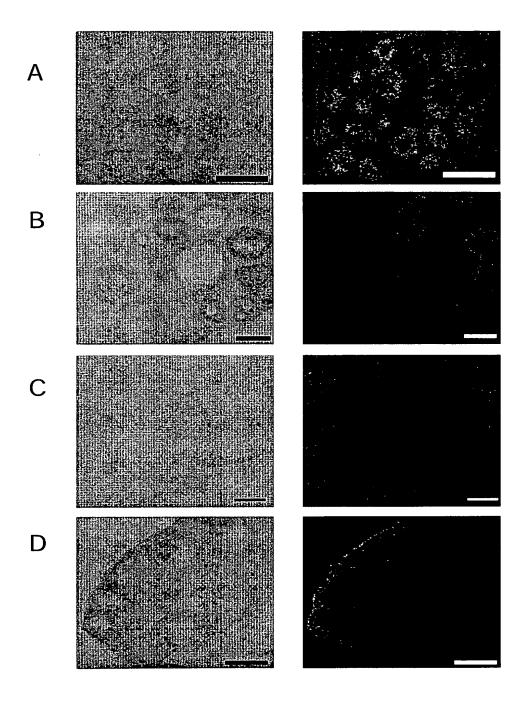
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101 HSEVAAYDSGRPGPLLGRPAMLASHMSALSQSQLISQMGLRSGIAHSSPS 150
151 PPGSKSATPSPSSSTQEEESDAHFKISGEKRPSTDPGKKAKNPKKKKKKD 200
201 PNEPQKPVSAYALFFRDTQAAIKGQNPSATFGDVSKIVASMWDSLGEEQK 250
251 QAYKRKTEAAKKEYLKALAAYRASLVSKSPPDQGEAKNAQANPPAKMLPP 300
301 KQPMYAMPGLASFLTPSDLQAFRSAASPASLARTLGSKALLPGLSTSPPP 350
351 PSFPLSPSLHQQLPLPPHAQGTLLSPPLSMSPAPQPPVLPAPMALQVQLA 400
401 MSPSPPGPQDFPHISDFPSGSGSRSPGPSNPSSSGDWDGSYPSGERGLGT 450
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Fig. 2



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Fig. 3



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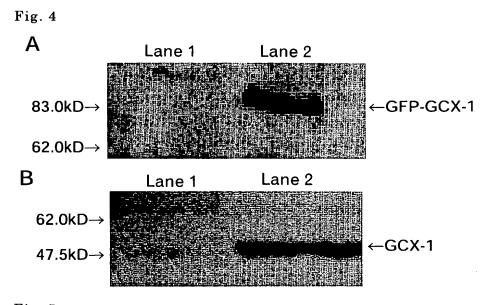
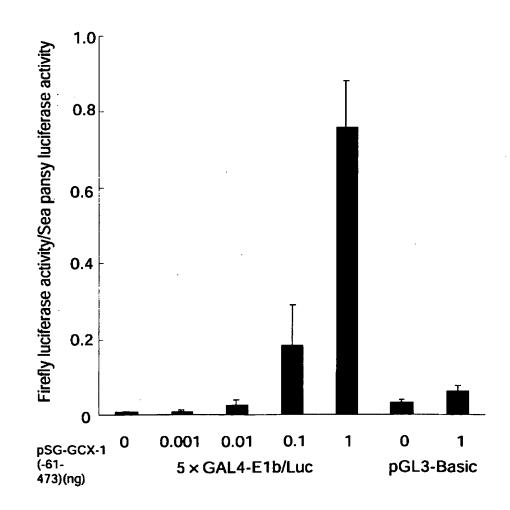


Fig. 5



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